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L5   ANSWER 1 OF 3  HCAPLUS  COPYRIGHT 2009 ACS on STN
AN   2004:502191  HCAPLUS <<LOGINID::20090202>>
DN   141:122298
TI   Identification of Peptides That Antagonize Formyl Peptide Receptor-Like
     1-Mediated Signaling
AU   Bae, Yoe-Sik; Lee, Ha Young; Jo, Eun Jin; Kim, Jung Im; Kang, Hyun-Kyu;
     Ye, Richard D.; Kwak, Jong-Young; Ryu, Sung Ho
CS   Medical Research Center for Cancer Molecular Therapy and Department of
     Biochemistry, College of Medicine, Dong-A University, Pusan, 602-714, S.
     Korea
SO   Journal of Immunology (  ***2004***  ), 173(1), 607-614
     CODEN: JOIMA3; ISSN: 0022-1767
PB   American Association of Immunologists
DT   Journal
LA   English
AB   Formyl peptide receptor-like 1 (FPRL1) is an important classical
     chemoattractant receptor that is expressed in phagocytic cells in the
     peripheral blood and brain.  Recently, various novel agonists have been
     identified from several origins, such as host-derived mols.  Activation of
     FPRL1 is closely related to inflammatory responses in the host defense
     mechanism and neurodegenerative disorders.  Here, the authors identified
     several novel peptides by screening hexapeptide libraries that inhibit the
     binding of one of FPRL1 agonists [Trp-Lys-Tyr-Met-Val-D-Met-CONH2
     (WKYMVm)] to its specific receptor, FPRL1, in RBL-2H3 cells.  Among the
     novel peptides, Trp-Arg-Trp-Trp-Trp-Trp-CONH2 [WRWWWW (WRW4)] showed the
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     resulting in the complete inhibition of the intracellular calcium
     increase, extracellular signal-regulated kinase activation, and
     chemotactic migration of cells toward WKYMVm.  For the receptor
     specificity of WRW4 to the FPR family, the authors obsd. that WRW4
     specifically inhibit the increase in intracellular calcium by the FPRL1
     agonists MMK-1, amyloid .beta.42 (A.beta.42) peptide, and F peptide, but
     not by the FPR agonist, fMLF.  To investigate the effect of WRW4 on
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     effect on A.beta.42 peptide in human neutrophils.  A.beta.42
     peptide-induced superoxide generation and chemotactic migration of
     neutrophils were inhibited by WRW4, which also completely inhibited the
     internalization of A.beta.42 peptide in human macrophages.  WRW4 is the
     first specific FPRL1 antagonist and is expected to be useful in the study
     of FPRL1 signaling and in the development of drugs against FPRL1-related
     diseases.
RE.CNT  41    THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5   ANSWER 2 OF 3  HCAPLUS  COPYRIGHT 2009 ACS on STN DUPLICATE 1
AN   2000:754713  HCAPLUS <<LOGINID::20090202>>
DN   133:330539
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TI Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis

IN Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.

PA Ceres Inc., USA

SO Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 43

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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	US 1999-132487P	P	19990506		
	US 1999-132863P	P	19990507		
	US 1999-134256P	P	19990511		
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	US 1999-135353P	P	19990521		
	US 1999-135629P	P	19990524		
	US 1999-136021P	P	19990525		
	US 1999-136392P	P	19990527		
	US 1999-136782P	P	19990528		
	US 1999-137222P	P	19990601		
	US 1999-137528P	P	19990603		

US 1999-137502P P 19990604
US 1999-137724P P 19990607
US 1999-138094P P 19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present exptl. but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133162185280 necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L5 ANSWER 3 OF 3 HCAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:9190 HCAPLUS <<LOGINID::20090202>>
DN 132:103595
TI Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
AU Mayer, K.; Schuller, C.; Wambutt, R.; Murphy, G.; Volckaert, G.; Pohl, T.; Dusterhoft, A.; Stiekema, W.; Entlan, K.-D.; Terryn, N.; Harris, B.; Ansorge, W.; Brandt, P.; Grivell, L.; Rieger, M.; Weichselgartner, M.; De Simone, V.; Obermaier, B.; Mache, R.; Muller, M.; Kreis, M.; Delseny, M.; Puigdomenech, P.; Watson, M.; Schmidtheini, T.; Reichert, B.; Portatelle, D.; Perez-Alonso, M.; Boutry, M.; Bancroft, I.; Vos, P.; Hoheisel, J.; Zimmermann, W.; Wedler, H.; Ridley, P.; Langham, S.-A.; McCullagh, B.; Bilham, L.; Robben, J.; Van Der Schueren, J.; Grymonprez, B.; Chuang, Y.-J.; Vandenbussche, F.; Braeken, M.; Weltjens, I.; Voet, M.; Bastiaens, I.; Aert, R.; Defoor, E.; Weitzenegger, T.; Bothe, G.; Ramsperger, U.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Peters, S.; Van Staveren, M.; Dirkse, W.; Mooijman, P.; Klein Lankhorst, R.; Rose, M.; Haut, J.; Kotter, P.; Berneiser, S.; Hempel, S.; Feldpausch, M.; Lamberth, S.; Van Den Daele, H.; De Keyser, A.; Buysshaert, C.; Gielen, J.; Villarroel, R.; De Clercq, R.; Van Montagu, M.; Rogers, J.; Cronin, A.; Quail, M.; Bray-Allen, S.; Clark, L.; Doggett, J.; Hall, S.; Kay, M.; Lennard, N.; McLay, K.; Mayes, R.; Pettett, A.; Rajandream, M.-A.; Lyne, M.; Benes, V.; Rechmann, S.; Borkova, D.; Blocker, H.; Scharfe, M.; Grimm, M.; Lohnert, T.-H.; Dose, S.; De Haan, M.; Maarse, A.; Schafer, M.; Muller-Auer, S.; Gabel, C.; Fuchs, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; Neumann, S.; Argiriou, A.; Vitale, D.; Liguori, R.; Piravandi, E.; Massenet, O.; Quigley, F.; Clabauld, G.; Mundlein, A.; Felber, R.; Schnabl, S.; Hiller, R.; Schmidt, W.; Lecharny, A.; Aubourg, S.; Chefdor, F.; Cooke, R.; Berger, C.; Montfort, M.; Casacuberta, E.; Gibbons, T.; Weber, N.; Vandenbol, M.; Bargues, M.; Terol, J.; Torres, A.; Perez-Perez, A.; Purnelle, B.; Bent, E.; Johnson, S.; Tacon, D.; Jesse, T.; Heijnen, L.; Schwarz, S.; Scholler, P.; Heber, S.; Francs, P.; Bielke, C.; Frishman, D.; Haase, D.; Lemcke, K.; Mewes, H. W.; Stocker, S.; Zaccaria, P.; Bevan, M.; Wilson, R. K.; De La Bastide, M.; Habermann, K.; Parnell, L.; Dedhia, N.; Gnoj, L.; Schutz, K.; Huang, E.; Spiegel, L.; Sehkon, M.; Murray, J.; Sheet, P.; Cordes, M.; Abu-Threideh, J.; Stoneking, T.; Kalicki, J.; Graves, T.; Harmon, G.; Edwards, J.; Latrelle, P.; Courtney, L.; Cloud, J.; Abbott, A.; Scott, K.; Johnson, D.; Minx, P.; Bentley, D.; Fulton, B.; Miller, N.; Greco, T.; Kemp, K.; Kramer, J.; Fulton, L.; Mardis, E.; Dante, M.; Pepin, K.; Hillier, L.; Nelson, J.; Spieth, J.; Ryan, E.; Andrews, S.; Geisel, C.; Layman, D.; Du, H.; Ali, J.; Berghoff, A.; Jones, K.; Drone, K.; Cotton, N.; Joshu, C.; Antonoiu, B.; Zidanic, M.; Strong, C.; Sun, H.; Lamar, B.; Yordan, C.; Ma, P.; Zhong, J.; Preston, R.; Vil, D.; Shekher, M.; Matero, A.; Shah, R.; Swaby, I'K.; O'Shaughnessy, A.; Rodriguez, M.; Hoffman, J.; Till, S.; Granat, S.; Shohdy, N.; Hasegawa, A.; Hameed, A.; Lodhi, M.; Johnson, A.; Chen, E.; Marra, M.; Martienssen, R.; McCombie, W. R.
CS GSF-Forschungszentrum f. Umwelt u. Gesundheit, Munich Information Center for Protein Sequences am Max-Planck-Institut f. Biochemie, D-82152, Germany
SO Nature (London) (***1999***), 402(6763), 769-777
CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB The higher plant Arabidopsis thaliana is an important model for identifying plant genes and detg. their function. To assist biol. investigations and to define chromosome structure, a coordinated effort to sequence the Arabidopsis genome was initiated in late 1996. This report describes one of the first milestones of this project, the sequence of chromosome 4. Anal. of 17.38 megabases of unique sequence, representing

```
     about 17% of the genome, reveals 3744 protein coding genes, 81 tRNAs, and
     numerous repeat elements.  Heterochromatic regions surrounding the
     putative centromere, which has not yet been completely sequenced, are
     characterized by an increased frequency of a variety of repeats, new
     repeats, reduced recombination, lowered gene d., and lowered gene
     expression.  Roughly 60% of the predicted protein-coding genes have been
     functionally characterized on the basis of their homol. to known genes.
     Many genes encode predicted proteins that are homologous to human and
     Caenorhabditis elegans proteins.
RE.CNT  50    THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT


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L6   ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2009 ACS on STN
AN   2004:502191  HCAPLUS <<LOGINID::20090202>>
DN   141:122298
TI   Identification of Peptides That Antagonize Formyl Peptide Receptor-Like
     1-Mediated Signaling
AU   Bae, Yoe-Sik; Lee, Ha Young; Jo, Eun Jin; Kim, Jung Im; Kang, Hyun-Kyu;
     Ye, Richard D.; Kwak, Jong-Young; Ryu, Sung Ho
CS   Medical Research Center for Cancer Molecular Therapy and Department of
     Biochemistry, College of Medicine, Dong-A University, Pusan, 602-714, S.
     Korea
SO   Journal of Immunology (  ***2004***  ), 173(1), 607-614
     CODEN: JOIMA3; ISSN: 0022-1767
PB   American Association of Immunologists
DT   Journal
LA   English
AB   Formyl peptide receptor-like 1 (FPRL1) is an important classical
     chemoattractant receptor that is expressed in phagocytic cells in the
     peripheral blood and brain.  Recently, various novel agonists have been
     identified from several origins, such as host-derived mols.  Activation of
     FPRL1 is closely related to inflammatory responses in the host defense
     mechanism and neurodegenerative disorders.  Here, the authors identified
     several novel peptides by screening hexapeptide libraries that inhibit the
     binding of one of FPRL1 agonists [Trp-Lys-Tyr-Met-Val-D-Met-CONH2
     (WKYMVm)] to its specific receptor, FPRL1, in RBL-2H3 cells.  Among the
     novel peptides, Trp-Arg-Trp-Trp-Trp-Trp-CONH2 [WRWWWW (WRW4)] showed the
     most potent activity in terms of inhibiting WKYMVm binding to FPRL1.  The
     authors also found that WRW4 inhibited the activation of FPRL1 by WKYMVm,
     resulting in the complete inhibition of the intracellular calcium
     increase, extracellular signal-regulated kinase activation, and
     chemotactic migration of cells toward WKYMVm.  For the receptor
     specificity of WRW4 to the FPR family, the authors obsd. that WRW4
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     agonists MMK-1, amyloid .beta.42 (A.beta.42) peptide, and F peptide, but
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     diseases.
RE.CNT  41    THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
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FILE 'CAPLUS' ENTERED AT 13:30:07 ON 02 FEB 2009
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AN   2004:502191  CAPLUS <<LOGINID::20090202>>
DN   141:122298
TI   Identification of Peptides That Antagonize Formyl Peptide Receptor-Like
     1-Mediated Signaling
AU   Bae, Yoe-Sik; Lee, Ha Young; Jo, Eun Jin; Kim, Jung Im; Kang, Hyun-Kyu;
     Ye, Richard D.; Kwak, Jong-Young; Ryu, Sung Ho
CS   Medical Research Center for Cancer Molecular Therapy and Department of
     Biochemistry, College of Medicine, Dong-A University, Pusan, 602-714, S.
     Korea
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     CODEN: JOIMA3; ISSN: 0022-1767
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DT   Journal
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     binding of one of FPRL1 agonists [Trp-Lys-Tyr-Met-Val-D-Met-CONH2
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     of FPRL1 signaling and in the development of drugs against FPRL1-related
     diseases.
RE.CNT  41    THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN   2004:502191  CAPLUS <<LOGINID::20090202>>
DN   141:122298
TI   Identification of Peptides That Antagonize Formyl Peptide Receptor-Like
     1-Mediated Signaling
AU   Bae, Yoe-Sik; Lee, Ha Young; Jo, Eun Jin; Kim, Jung Im; Kang, Hyun-Kyu;
     Ye, Richard D.; Kwak, Jong-Young; Ryu, Sung Ho
CS   Medical Research Center for Cancer Molecular Therapy and Department of
     Biochemistry, College of Medicine, Dong-A University, Pusan, 602-714, S.
     Korea
SO   Journal of Immunology (  ***2004***  ), 173(1), 607-614
     CODEN: JOIMA3; ISSN: 0022-1767
PB   American Association of Immunologists
DT   Journal
LA   English
AB   Formyl peptide receptor-like 1 (FPRL1) is an important classical
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     resulting in the complete inhibition of the intracellular calcium
     increase, extracellular signal-regulated kinase activation, and
     chemotactic migration of cells toward WKYMVm.  For the receptor
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     not by the FPR agonist, fMLF.  To investigate the effect of WRW4 on
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     effect on A.beta.42 peptide in human neutrophils.  A.beta.42
     peptide-induced superoxide generation and chemotactic migration of
     neutrophils were inhibited by WRW4, which also completely inhibited the
     internalization of A.beta.42 peptide in human macrophages.  WRW4 is the
     first specific FPRL1 antagonist and is expected to be useful in the study
     of FPRL1 signaling and in the development of drugs against FPRL1-related
     diseases.
RE.CNT  41    THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD
              ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9   ANSWER 2 OF 3  CAPLUS  COPYRIGHT 2009 ACS on STN  DUPLICATE 1
AN   2000:754713  CAPLUS <<LOGINID::20090202>>
DN   133:330539
TI   Sequence-determined DNA fragments and corresponding encoded polypeptides
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IN   Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian,
     Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PA   Ceres Inc., USA
SO   Eur. Pat. Appl., 339 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
FAN.CNT 43
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     EP 1054060          A2     20001122    EP 2000-304161         20000517 <--
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            IE, SI, LT, LV, FI, RO
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     US 1999-145918P     P      19990727
     US 1999-145951P     P      19990728
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AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133162185280 necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

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TI Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
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CS GSF-Forschungszentrum f. Umwelt u. Gesundheit, Munich Information Center for Protein Sequences am Max-Planck-Institut f. Biochemie, D-82152, Germany

SO Nature (London) (***1999***), 402(6763), 769-777
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AB The higher plant Arabidopsis thaliana is an important model for identifying plant genes and detg. their function. To assist biol. investigations and to define chromosome structure, a coordinated effort to sequence the Arabidopsis genome was initiated in late 1996. This report describes one of the first milestones of this project, the sequence of chromosome 4. Anal. of 17.38 megabases of unique sequence, representing about 17% of the genome, reveals 3744 protein coding genes, 81 tRNAs, and numerous repeat elements. Heterochromatic regions surrounding the putative centromere, which has not yet been completely sequenced, are characterized by an increased frequency of a variety of repeats, new repeats, reduced recombination, lowered gene d., and lowered gene expression. Roughly 60% of the predicted protein-coding genes have been functionally characterized on the basis of their homol. to known genes. Many genes encode predicted proteins that are homologous to human and Caenorhabditis elegans proteins.

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